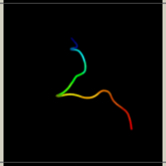
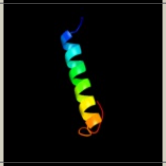
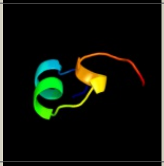
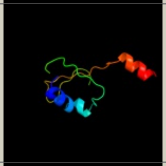
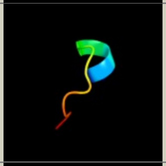
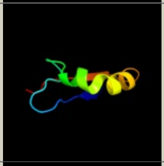
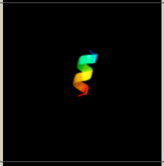
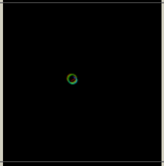
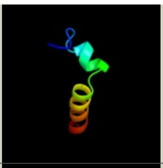
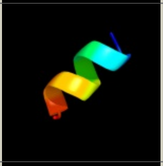
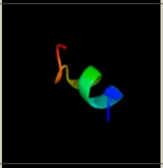
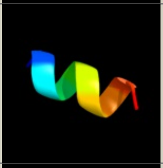
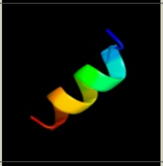
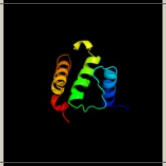
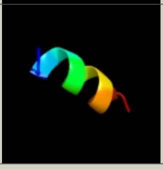
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P76938
Date	Thu Jan 5 12:25:24 GMT 2012
Unique Job ID	9967eae4bf3f8516

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hftA_	Alignment		50.8	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**wbms, polysaccharide deacetylase involved in o-antigen **PDBTitle:** crystal structure of a putative polysaccharide deacetylase involved in2 o-antigen biosynthesis (wbms, bb0128) from bordetella bronchiseptica3 at 1.90 a resolution
2	d1h3ia2	Alignment		47.5	36	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
3	c3pmiC_	Alignment		42.9	23	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**pwwp domain-containing protein mum1; **PDBTitle:** pwwp domain of human mutated melanoma-associated antigen 1
4	d1g12a_	Alignment		32.0	41	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Fungal zinc peptidase
5	c1su3A_	Alignment		28.3	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interstitial collagenase; **PDBTitle:** x-ray structure of human prommp-1: new insights into2 collagenase action
6	c3cskA_	Alignment		26.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable dipeptidyl-peptidase 3; **PDBTitle:** structure of dpp iii from saccharomyces cerevisiae
7	d2pu9a1	Alignment		23.1	31	**Fold:**Ferredoxin thioredoxin reductase (FTR), catalytic beta chain **Superfamily:**Ferredoxin thioredoxin reductase (FTR), catalytic beta chain **Family:**Ferredoxin thioredoxin reductase (FTR), catalytic beta chain
8	c1ycdA_	Alignment		22.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical 27.3 kda protein in aap1-smf2 **PDBTitle:** crystal structure of yeast fsh1/yhr049w, a member of the2 serine hydrolase family
9	d1lmla_	Alignment		21.4	27	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Leishmanolysin
10	c1om8A_	Alignment		20.6	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serralysin; **PDBTitle:** crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallyzed with 10 mm edta
11	d1xuca1	Alignment		19.4	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain

12	c3mc4A_	Alignment		19.3	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ww/rsp5/wwp domain:bacterial transferase **PDBTitle:** crystal structure of ww/rsp5/wwp domain: bacterial2 transferase hexapeptide repeat: serine o-acetyltransferase3 from brucella melitensis
13	c2j83B_	Alignment		18.6	60	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ulilysin; **PDBTitle:** ulilysin metalloprotease in complex with batimastat.
14	c3c18B_	Alignment		18.2	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nucleotidyltransferase-like protein; **PDBTitle:** crystal structure of nucleotidyltransferase-like protein2 (zp_00538802.1) from exiguobacterium sibiricum 255-15 at 1.90 a3 resolution
15	d1sata2	Alignment		17.7	40	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
16	d1i76a_	Alignment		17.5	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
17	c1slmA_	Alignment		17.3	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
18	c3cqbB_	Alignment		17.2	67	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable protease htpx homolog; **PDBTitle:** crystal structure of heat shock protein htpx domain from vibrio2 parahaemolyticus rimd 2210633
19	d1dxxa2	Alignment		17.0	15	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
20	d1cxva_	Alignment		16.9	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
21	d1tqha_	Alignment	not modelled	16.8	27	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/lipase
22	c2x3bB_	Alignment	not modelled	16.7	35	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**toxic extracellular endopeptidase; **PDBTitle:** asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
23	c3dtkA_	Alignment	not modelled	16.6	38	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**irre protein; **PDBTitle:** crystal structure of the irre protein, a central regulator2 of dna damage repair in deinococcaceae
24	d1cgla_	Alignment	not modelled	16.2	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
25	d1q3aa_	Alignment	not modelled	16.2	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
26	d1hova_	Alignment	not modelled	16.2	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
27	d1k7ia2	Alignment	not modelled	16.2	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
28	d1g9ka2	Alignment	not modelled	16.2	40	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
						Fold: Zincin-like

29	d1eaka2	Alignment	not modelled	16.1	25	**Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
30	d1poca_	Alignment	not modelled	15.9	24	**Fold:**Phospholipase A2, PLA2 **Superfamily:**Phospholipase A2, PLA2 **Family:**Insect phospholipase A2
31	c2jsdA_	Alignment	not modelled	15.5	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-20; **PDBTitle:** solution structure of mmp20 complexed with nngh
32	d1hfca_	Alignment	not modelled	15.2	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
33	d1rm8a_	Alignment	not modelled	15.1	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
34	d1kapp2	Alignment	not modelled	14.9	40	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
35	d1bqqm_	Alignment	not modelled	14.7	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
36	c3ls2D_	Alignment	not modelled	14.6	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-formylglutathione hydrolase; **PDBTitle:** crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125
37	c1zmhA_	Alignment	not modelled	14.3	71	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 2; **PDBTitle:** crystal structure of human neutrophil peptide 2, hnp-2 (variant gly16-2 > d-ala)
38	c1zmhD_	Alignment	not modelled	14.3	71	**PDB header:**antimicrobial protein **Chain:** D: **PDB Molecule:**neutrophil defensin 2; **PDBTitle:** crystal structure of human neutrophil peptide 2, hnp-2 (variant gly16-2 > d-ala)
39	c1zmkA_	Alignment	not modelled	14.3	71	**PDB header:**antimicrobial protein **Chain:** C: **PDB Molecule:**neutrophil defensin 2; **PDBTitle:** crystal structure of human alpha-defensin-2 (variant gly16-> d-ala), p2 42 21 2 space group
40	c1zmiC_	Alignment	not modelled	14.3	71	**PDB header:**antimicrobial protein **Chain:** C: **PDB Molecule:**neutrophil defensin 2; **PDBTitle:** crystal structure of human alpha_defensin-2 (variant gly16->d-ala), p2 32 2 1 space group)
41	c1zmiA_	Alignment	not modelled	14.3	71	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 2; **PDBTitle:** crystal structure of human alpha_defensin-2 (variant gly16->d-ala), p2 32 2 1 space group)
42	c1zmkB_	Alignment	not modelled	14.3	71	**PDB header:**antimicrobial protein **Chain:** B: **PDB Molecule:**neutrophil defensin 2; **PDBTitle:** crystal structure of human alpha-defensin-2 (variant gly16-> d-ala), p2 42 21 2 space group
43	c1zmhC_	Alignment	not modelled	14.3	71	**PDB header:**antimicrobial protein **Chain:** C: **PDB Molecule:**neutrophil defensin 2; **PDBTitle:** crystal structure of human neutrophil peptide 2, hnp-2 (variant gly16-2 > d-ala)
44	c1zmiB_	Alignment	not modelled	14.3	71	**PDB header:**antimicrobial protein **Chain:** B: **PDB Molecule:**neutrophil defensin 2; **PDBTitle:** crystal structure of human alpha_defensin-2 (variant gly16->d-ala), p2 32 2 1 space group)
45	c1zmhB_	Alignment	not modelled	14.3	71	**PDB header:**antimicrobial protein **Chain:** B: **PDB Molecule:**neutrophil defensin 2; **PDBTitle:** crystal structure of human neutrophil peptide 2, hnp-2 (variant gly16-2 > d-ala)
46	c1zmiD_	Alignment	not modelled	14.3	71	**PDB header:**antimicrobial protein **Chain:** D: **PDB Molecule:**neutrophil defensin 2; **PDBTitle:** crystal structure of human alpha_defensin-2 (variant gly16->d-ala), p2 32 2 1 space group)
47	d1fbla2	Alignment	not modelled	14.1	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
48	d1y93a1	Alignment	not modelled	14.0	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
49	c3ba0A_	Alignment	not modelled	13.9	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrophage metalloelastase; **PDBTitle:** crystal structure of full-length human mmp-12
50	c3fcxA_	Alignment	not modelled	13.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**s-formylglutathione hydrolase; **PDBTitle:** crystal structure of human esterase d
51	c2wtmC_	Alignment	not modelled	13.6	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**est1e; **PDBTitle:** est1e from butyrivibrio proteoclasticus
52	d2hu7a1	Alignment	not modelled	13.5	20	**Fold:**7-bladed beta-propeller **Superfamily:**Peptidase/esterase 'gauge' domain **Family:**Acylamino-acid-releasing enzyme, N-terminal donain
53	c3hjdB_	Alignment	not modelled	13.5	71	**PDB header:**antimicrobial protein **Chain:** B: **PDB Molecule:**human neutrophil peptide 1; **PDBTitle:** x-ray structure of monomeric variant of hnp1
54	c3hjdA_	Alignment	not modelled	13.5	71	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**human neutrophil peptide 1; **PDBTitle:** x-ray structure of monomeric variant of hnp1
55	c2xs4A_	Alignment	not modelled	13.4	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**karilysin protease; **PDBTitle:** structure of karilysin catalytic mmp domain in complex with2 magnesium

56	c2cltB_	Alignment	not modelled	13.4	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**interstitial collagenase; **PDBTitle:** crystal structure of the active form (full-length) of human2 fibroblast collagenase.
57	d1mmqa_	Alignment	not modelled	13.3	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
58	c3lo4B_	Alignment	not modelled	13.3	71	**PDB header:**antimicrobial protein **Chain:** B: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (r24a mutant)
59	c3lo4A_	Alignment	not modelled	13.3	71	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (r24a mutant)
60	d1dfna_	Alignment	not modelled	13.3	71	**Fold:**Defensin-like **Superfamily:**Defensin-like **Family:**Defensin
61	c3lvxA_	Alignment	not modelled	13.2	71	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (i6a mutant)
62	c3lo6A_	Alignment	not modelled	13.2	71	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (w26aba mutant)
63	c3lo9B_	Alignment	not modelled	13.2	71	**PDB header:**antimicrobial protein **Chain:** B: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (w26ahp mutant)
64	c3lo6B_	Alignment	not modelled	13.2	71	**PDB header:**antimicrobial protein **Chain:** B: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (w26aba mutant)
65	c3lo9A_	Alignment	not modelled	13.2	71	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (w26ahp mutant)
66	c3lvxB_	Alignment	not modelled	13.1	71	**PDB header:**antimicrobial protein **Chain:** B: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (i6a mutant)
67	c3gnyB_	Alignment	not modelled	13.1	71	**PDB header:**antimicrobial protein **Chain:** B: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (hnp1)
68	c3h6cB_	Alignment	not modelled	12.9	71	**PDB header:**antimicrobial protein **Chain:** B: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (mutant gln22ala)
69	c3h6cA_	Alignment	not modelled	12.9	71	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (mutant gln22ala)
70	c3lo2B_	Alignment	not modelled	12.8	71	**PDB header:**antimicrobial protein **Chain:** B: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (y21a mutant)
71	c3lo2A_	Alignment	not modelled	12.8	71	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (y21a mutant)
72	c3lo1A_	Alignment	not modelled	12.8	71	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (y16a mutant)
73	c2zagB_	Alignment	not modelled	12.8	80	**PDB header:**transferase **Chain:** B: **PDB Molecule:**oligosaccharyl transferase stt3 subunit related protein; **PDBTitle:** crystal structure of the semet-substituted soluble domain of stt3 from2 p. furiosus
74	c3noyA_	Alignment	not modelled	12.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** crystal structure of ispg (gcpe)
75	d1vlta_	Alignment	not modelled	12.7	27	**Fold:**Four-helical up-and-down bundle **Superfamily:**Aspartate receptor, ligand-binding domain **Family:**Aspartate receptor, ligand-binding domain
76	d1hy7a_	Alignment	not modelled	12.4	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
77	d1xdna_	Alignment	not modelled	12.3	15	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**RNA ligase
78	c1i8yA_	Alignment	not modelled	12.2	56	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**granulin-1; **PDBTitle:** semi-automatic structure determination of the cg1 3-302 peptide based on aria
79	d1i8ya_	Alignment	not modelled	12.2	56	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Granulin repeat **Family:**Granulin repeat
80	d1sr9a1	Alignment	not modelled	11.9	32	**Fold:**RuvA C-terminal domain-like **Superfamily:**post-HMGL domain-like **Family:**DmpG/LeuA communication domain-like
81	d2ejqa1	Alignment	not modelled	11.9	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
						Fold: Zincin-like

82	d2ovxa1	Alignment	not modelled	11.8	25	**Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
83	c3o0lB_	Alignment	not modelled	11.3	43	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a pfam duf1425 family member (shew_1734) from2 shewanella sp. pv-4 at 1.81 a resolution
84	d1m0wa1	Alignment	not modelled	11.3	8	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Eukaryotic glutathione synthetase, substrate-binding domain
85	c3loeA_	Alignment	not modelled	11.2	71	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (f28a mutant)
86	c3gnyA_	Alignment	not modelled	11.0	71	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (hnp1)
87	c1xqhE_	Alignment	not modelled	11.0	29	**PDB header:**transferase **Chain:** E: **PDB Molecule:**histone-lysine n-methyltransferase, h3 lysine-4 **PDBTitle:** crystal structure of a ternary complex of the2 methyltransferase set9 (also known as set7/9) with a p533 peptide and sah
88	c2pm4A_	Alignment	not modelled	10.9	57	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1 (hnp-1) (hp-1) (hp1) (defensin, alpha **PDBTitle:** human alpha-defensin 1 (multiple arg->lys mutant)
89	d1hv5a_	Alignment	not modelled	10.8	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
90	d1qiba_	Alignment	not modelled	10.8	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
91	c2d99A_	Alignment	not modelled	10.8	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna
92	d1pv1a_	Alignment	not modelled	10.7	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical esterase YJL068C
93	d1jwya1	Alignment	not modelled	10.7	80	**Fold:**SH3-like barrel **Superfamily:**Myosin S1 fragment, N-terminal domain **Family:**Myosin S1 fragment, N-terminal domain
94	c3f67A_	Alignment	not modelled	10.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative dienelactone hydrolase; **PDBTitle:** crystal structure of putative dienelactone hydrolase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
95	c2dzrA_	Alignment	not modelled	10.5	35	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-067, a gtf2i domain in human2 cdna
96	c2hdwB_	Alignment	not modelled	10.3	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein pa2218; **PDBTitle:** crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
97	d1i0ua2	Alignment	not modelled	10.2	20	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**EGF/Laminin **Family:**EGF-type module
98	d2crna1	Alignment	not modelled	10.1	50	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
99	d3bz7a1	Alignment	not modelled	10.0	80	**Fold:**SH3-like barrel **Superfamily:**Myosin S1 fragment, N-terminal domain **Family:**Myosin S1 fragment, N-terminal domain